

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Nehls, Michael
Friedrich, Glenn
Scoville, John
Zambrowicz, Brian
Sands, Arthur T.

<120> Novel Human 7TM Proteins and Receptors and
Polynucleotides Encoding the Same

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<150> US 60/153,366

<151> 1999-09-10

<150> US 60/165,510

<151> 1999-11-15

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<210> 4

<211> 1221

<212> PRT

<213> homo sapiens

<400> 4

Met Phe Arg Ser Asp Arg Met Trp Ser Cys His Trp Lys Trp Lys Pro

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Ser Ala Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro			
35	40	45	
Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser			
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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln			
65	70	75	80
Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr			
85	90	95	
Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly			
100	105	110	
Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His			
115	120	125	
Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala			
130	135	140	
Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu			
145	150	155	160
Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser			
165	170	175	
Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val			
180	185	190	
Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser			
195	200	205	
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu			
210	215	220	
Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys			
225	230	235	240
Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val			
245	250	255	
Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr			
260	265	270	
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn			
275	280	285	
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys			
290	295	300	
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys			
305	310	315	320
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp			
325	330	335	
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser			
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Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu			
355	360	365	
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Ala Thr Val Asn Ser			
370	375	380	
Pro Ser Thr Thr Pro Pro Thr Val Thr Thr Asn Met Pro Val Thr Asn			
385	390	395	400
Arg Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val			
405	410	415	
Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys			
420	425	430	
Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val			
435	440	445	
Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile			

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Lys Val Lys Arg Ser	Leu Glu Asp Glu Pro Arg	Leu Val Leu Trp Ala		
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Leu Leu Val Tyr Asn	Ala Thr Asn Asn Thr Asn	Leu Glu Gly Lys Ile		
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Ile Gln Gln Lys Leu	Leu Lys Asn Asn Glu Ser	Leu Asp Glu Gly Leu		
500	505	510		
Arg Leu His Thr Val	Asn Val Arg Gln Leu Gly	His Cys Leu Ala Met		
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Glu Glu Pro Lys Gly	Tyr Tyr Trp Pro Ser Ile	Gln Pro Ser Glu Tyr		
530	535	540		
Val Leu Pro Cys Pro	Asp Lys Pro Gly Phe Ser	Ala Ser Arg Ile Cys		
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Phe Tyr Asn Ala Thr	Asn Pro Leu Val Thr Tyr	Trp Gly Pro Val Asp		
565	570	575		
Ile Ser Asn Cys Leu	Lys Glu Ala Asn Glu Val	Ala Asn Gln Ile Leu		
580	585	590		
Asn Leu Thr Ala Asp	Gly Gln Asn Leu Thr Ser	Ala Asn Ile Thr Asn		
595	600	605		
Ile Val Glu Gln Val	Lys Arg Ile Val Asn Lys	Glu Glu Asn Ile Asp		
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Ser Ser Asp Ser Asp	Leu Leu Glu Ser Ser	Glu Ala Leu Lys Thr		
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Ile Asp Glu Leu Ala	Phe Lys Ile Asp Leu	Asn Ser Thr Ser His Val		
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Asn Ile Thr Thr Arg	Asn Leu Ala Leu Ser	Val Ser Ser Leu Leu Pro		
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Gly Thr Asn Ala Ile	Ser Asn Phe Ser Ile Gly	Leu Pro Ser Asn Asn		
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Glu Ser Tyr Phe Gln	Met Asp Phe Glu Ser Gly	Gln Val Asp Pro Leu		
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Ala Ser Val Ile Leu	Pro Pro Asn Leu Leu Glu	Asn Leu Ser Pro Glu		
725	730	735		
Asp Ser Val Leu Val	Arg Arg Ala Gln Phe	Thr Phe Phe Asn Lys Thr		
740	745	750		
Gly Leu Phe Gln Asp	Val Gly Pro Gln Arg Lys	Thr Leu Val Ser Tyr		
755	760	765		
Val Met Ala Cys Ser	Ile Gly Asn Ile Thr Ile	Gln Asn Leu Lys Asp		
770	775	780		
Pro Val Gln Ile Lys	Ile Lys His Thr Arg Thr	Gln Glu Val His His		
785	790	795	800	
Pro Ile Cys Ala Phe	Trp Asp Leu Asn Lys Asn	Lys Ser Phe Gly Gly		
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Trp Asn Thr Ser Gly	Cys Val Ala His Arg Asp	Ser Asp Ala Ser Glu		
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Thr Val Cys Leu Cys	Asn His Phe Thr His Phe	Gly Val Leu Met Asp		
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Leu Pro Arg Ser Ala	Ser Gln Leu Asp Ala Arg	Asn Thr Lys Val Leu		
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Thr Phe Ile Ser Tyr	Ile Gly Cys Gly Ile Ser	Ala Ile Phe Ser Ala		
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Ala Thr Leu Leu Thr	Tyr Val Ala Phe Glu Lys	Leu Arg Arg Asp Tyr		
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Pro Ser Lys Ile Leu	Met Asn Leu Ser Thr Ala	Leu Leu Phe Leu Asn		

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Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly		
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Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr		
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Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val		
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Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile		
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Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser		
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Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys		
995	1000	1005
Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr		
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Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe		
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Ile Val Val Met Val Glu Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn		
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Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser		
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Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp		
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Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser		
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Leu Gln Gly Leu Phe Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn		
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Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu		
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Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys		
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Ser Ser Asp Asn Leu Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser		
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Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr		
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Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu His Ser Phe		
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<211> 2157

<212> DNA

<213> homo sapiens

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<211> 718

<212> PRT

<213> homo sapiens

<400> 6

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			20					25					30		
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
			35				40						45		
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65						70				75				80	
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
				85					90					95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
			100				105						110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser

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			180					185					190				
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser		
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu		
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Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys		
	225				230				235						240		
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val		
			245				250						255				
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr		
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn		
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys		
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Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys		
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Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser		
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser		
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Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn		
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Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val		
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Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile		
	450					455					460						
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala		
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Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile		
			485					490					495				
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu		
			500					505					510				
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Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr		
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Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys		
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			580					585					590				
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		595					600					605					
Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	Glu	Asn	Ile	Asp		

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Ile Thr Leu Gly Ser	Thr Leu Met Asn Ile Phe	Ser Asn Ile Leu Ser		
625	630	635	640	
Ser Ser Asp Ser Asp	Leu Leu Glu Ser Ser Ser	Glu Ala Leu Lys Thr		
	645	650	655	
Ile Asp Glu Leu Ala Phe Lys Ile	Asp Leu Asn Ser Thr Ser His Val			
	660	665	670	
Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val	Ser Ser Leu Leu Pro			
	675	680	685	
Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly	Leu Pro Ser Asn Asn			
	690	695	700	
Glu Ser Tyr Phe Gln Val Met Ser Gln Trp Phe	Leu Ser Phe			
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<400> 7

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<213> homo sapiens

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<213> homo sapiens

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<211> 1250

<212> PRT

<213> homo sapiens

<400> 18

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Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	100	105	110
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	115	120	125
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	130	135	140
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	145	150	155
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	165	170	175
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	180	185	190
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	195	200	205
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	210	215	220
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	225	230	235
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	245	250	255
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	260	265	270
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Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val	435	440	445
Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile	450	455	460
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala	465	470	475
Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile	485	490	495

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Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu	
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Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp	
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 Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys
 995 1000 1005
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 Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe
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<211> 1221

<212> PRT

<213> homo sapiens

<400> 20

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Pro	Ser	Pro	Leu	Leu	Phe	Leu	Phe	Ala	Leu	Tyr	Ile	Met	Cys	Val	Pro
			20					25					30		
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
		35					40					45			
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65					70					75					80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
				85					90					95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
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Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135					140				
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
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Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
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Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser
	370					375					380				
Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn
385					390					395					400
Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val
				405					410					415	

Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys	420	425	430
Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val	435	440	445
Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile	450	455	460
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala	465	470	475
Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile	485	490	495
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu	500	505	510
Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys	Leu	Ala	Met	515	520	525
Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr	530	535	540
Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys	545	550	555
Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp	565	570	575
Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu	580	585	590
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Ser	Ser	Asp	Ser	Asp	Leu	Leu	Glu	Ser	Ser	Ser	Glu	Ala	Leu	Lys	Thr	645	650	655
Ile	Asp	Glu	Leu	Ala	Phe	Lys	Ile	Asp	Leu	Asn	Ser	Thr	Ser	His	Val	660	665	670
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Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	725	730	735
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Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr	755	760	765
Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp	770	775	780
Pro	Val	Gln	Ile	Lys	Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His	785	790	795
Pro	Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly	805	810	815
Trp	Asn	Thr	Ser	Gly	Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	820	825	830
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His	
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<212> DNA

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attgtggtaa	tggtgcagat	ctgtgggagg	aatggcaaga	gaagcaaccg	gaccctgaga	3180
gaagaagtgt	taaggaacct	gcgcagtgtg	gttagcttga	cctttctgtt	gggcatgaca	3240
tgggggtttg	cattctttgc	ctggggaccc	ttaaataatcc	ccttcatgta	cctcttctcc	3300
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<210> 24

<211> 1112

<212> PRT

<213> homo sapiens

<400> 24

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1				5				10						15	
Pro	Ser	Pro	Leu	Leu	Phe	Leu	Phe	Ala	Leu	Tyr	Ile	Met	Cys	Val	Pro
			20					25					30		
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
			35				40					45			
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65				70					75					80	
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			85					90					95		
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
			100				105						110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
			115				120					125			
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135					140				
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
145				150					155					160	
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
			165					170					175		
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
			180					185					190		

Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	195	200	205
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	210	215	220
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	225	230	235
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	245	250	255
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	260	265	270
Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn	275	280	285
Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys	290	295	300
Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys	305	310	315
Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp	325	330	335
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser	340	345	350
Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu	355	360	365
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser	370	375	380
Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn	385	390	395
Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val	405	410	415
Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys	420	425	430
Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val	435	440	445
Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile	450	455	460
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala	465	470	475
Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile	485	490	495
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu	500	505	510
Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys	Leu	Ala	Met	515	520	525
Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr	530	535	540
Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys	545	550	555
Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp	565	570	575
Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu	580	585	590
Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala	Asn	Ile	Thr	Asn	595	600	605
Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	Glu	Asn	Ile	Asp	610	615	620
Ile	Thr	Leu	Gly	Ser	Thr	Leu	Met	Asn	Ile	Phe	Ser	Asn	Ile	Leu	Ser	625	630	635

Ser	Ser	Asp	Ser	Asp	Leu	Leu	Glu	Ser	Ser	Ser	Glu	Ala	Leu	Lys	Thr
				645					650					655	
Ile	Asp	Glu	Leu	Ala	Phe	Lys	Ile	Asp	Leu	Asn	Ser	Thr	Ser	His	Val
			660					665					670		
Asn	Ile	Thr	Thr	Arg	Asn	Leu	Ala	Leu	Ser	Val	Ser	Ser	Leu	Leu	Pro
		675						680					685		
Gly	Thr	Asn	Ala	Ile	Ser	Asn	Phe	Ser	Ile	Gly	Leu	Pro	Ser	Asn	Asn
	690					695					700				
Glu	Ser	Tyr	Phe	Gln	Met	Asp	Phe	Glu	Ser	Gly	Gln	Val	Asp	Pro	Leu
705					710					715					720
Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn	Leu	Ser	Pro	Glu
				725						730					735
Asp	Ser	Val	Leu	Val	Arg	Arg	Ala	Gln	Phe	Thr	Phe	Phe	Asn	Lys	Thr
			740					745					750		
Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr
		755					760					765			
Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp
	770					775						780			
Pro	Val	Gln	Ile	Lys	Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His
785					790					795					800
Pro	Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly
				805						810					815
Trp	Asn	Thr	Ser	Gly	Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu
			820					825					830		
Thr	Val	Cys	Leu	Cys	Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp
		835					840					845			
Leu	Pro	Arg	Ser	Ala	Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu
	850					855					860				
Thr	Phe	Ile	Ser	Tyr	Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala
865					870					875					880
Ala	Thr	Leu	Leu	Thr	Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr
				885					890					895	
Pro	Ser	Lys	Ile	Leu	Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn
			900					905					910		
Leu	Leu	Phe	Leu	Leu	Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly
		915					920						925		
Leu	Cys	Ile	Ala	Val	Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr
		930					935					940			
Phe	Thr	Trp	Met	Gly	Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val
945					950					955					960
Lys	Val	Phe	Asn	Thr	Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile
			965						970					975	
Ile	Gly	Trp	Gly	Leu	Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser
			980					985					990		
Arg	Asn	Asn	Asn	Glu	Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys
		995					1000						1005		
Gly	Asp	Glu	Phe	Cys	Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr
	1010					1015						1020			
Cys	Ala	Gly	Tyr	Phe	Gly	Val	Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe
1025					1030					1035					1040
Ile	Val	Val	Met	Val	Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn
				1045					1050					1055	
Arg	Thr	Leu	Arg	Glu	Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser
			1060					1065					1070		
Leu	Thr	Phe	Leu	Leu	Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp
		1075					1080						1085		

Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser
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 Leu Gln Gly Lys Ile Asn Cys Thr
 1105 1110

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 <211> 1626
 <212> DNA
 <213> homo sapiens

<400> 25
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 aacaaaactg gacttttcca ggatgtagga ccccaaagaa aaactttagt gagttatgtg 180
 atggcgtgca gtattggaaa cattactatc cagaatctga aggatcctgt tcaaataaaa 240
 atcaaacata caagaactca ggaagtgcac catcccatct gtgccttctg ggatctgaac 300
 aaaaacaaaa gttttggagg atggaacacg tcaggatgtg ttgcacacag agattcagat 360
 gcaagtgaga cagtctgcct gtgtaaccac ttcacacact ttggagttct gatggacctt 420
 ccaagaagtg cctcacagtt agatgcaaga aacactaaag tcctcacttt catcagctat 480
 attgggtgtg gaatatctgc tattttttca gcagcaactc tcctgacata tgttgctttt 540
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 tgcattgctg ttgcagtcct gttgcatttc ttccttctgg caacctttac ctggatgggg 720
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 gatgaattct gttggattca agatccagtc atattttatg tgacctgtgc tgggtatttt 960
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 caaacatcaa tcatcctgt ccatcaggtc attgataagg tcaagggtta ttgcaatgct 1560
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<210> 26
 <211> 541
 <212> PRT
 <213> homo sapiens

<400> 26
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 20 25 30
 Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly Leu Phe Gln Asp
 35 40 45
 Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
 50 55 60
 Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
 65 70 75 80

Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His	Pro	Ile	Cys	Ala	Phe	
				85					90					95		
Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly	
			100					105					110			
Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys	
		115					120					125				
Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala	
	130					135					140					
Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr	
145					150					155					160	
Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Thr	Leu	Leu	Thr	
				165					170						175	
Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	
		180						185					190			
Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	
		195					200					205				
Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val	
	210					215					220					
Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly	
225					230					235					240	
Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	
				245					250					255		
Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu	
			260					265						270		
Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu	
		275					280						285			
Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys	
	290					295					300					
Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe	
305					310					315					320	
Gly	Val	Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe	Ile	Val	Val	Met	Val	
				325					330					335		
Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu	
			340					345					350			
Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	
	355						360					365				
Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile	
	370					375					380					
Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Leu	Phe	
385					390					395					400	
Ile	Phe	Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp	
				405					410					415		
Arg	Arg	His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Leu	Ala	Asp	Asn	Ser	Asp	
			420					425					430			
Trp	Ser	Lys	Thr	Ala	Thr	Asn	Ile	Ile	Lys	Lys	Ser	Ser	Asp	Asn	Leu	
		435					440						445			
Gly	Lys	Ser	Leu	Ser	Ser	Ser	Ser	Ile	Gly	Ser	Asn	Ser	Thr	Tyr	Leu	
	450					455					460					
Thr	Ser	Lys	Ser	Lys	Ser	Ser	Ser	Thr	Thr	Tyr	Phe	Lys	Arg	Asn	Ser	
465					470					475					480	
His	Thr	Asp	Ser	Ala	Ser	Met	Asp	Lys	Ser	Leu	Ser	Lys	Leu	Ala	His	
				485					490					495		
Ala	Asp	Gly	Asp	Gln	Thr	Ser	Ile	Ile	Pro	Val	His	Gln	Val	Ile	Asp	
			500					505					510			
Lys	Val	Lys	Gly	Tyr	Cys	Asn	Ala	His	Ser	Asp	Asn	Phe	Tyr	Lys	Asn	
		515					520					525				

Ile Ile Met Ser Asp Thr Phe Ser His Ser Thr Lys Phe
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<210> 27
 <211> 1539
 <212> DNA
 <213> homo sapiens

<400> 27
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 aacaaaactg gacttttcca ggatgtagga ccccaaagaa aaacttttagt gagttatgtg 180
 atggcgtgca gtattggaaa cattactatc cagaatctga aggatcctgt tcaaaataaaa 240
 atcaaacata caagaactca ggaagtgcac catcccatct gtgccttctg ggatctgaac 300
 aaaaacaaaa gttttggagg atggaacacg tcaggatgtg ttgcacacag agattcagat 360
 gaaagtgaga cagtctgcct gtgtaaccac ttcacacact ttggagtctt gatggacctt 420
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<210> 28
 <211> 512
 <212> PRT
 <213> homo sapiens

<400> 28
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 20 25 30
 Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly Leu Phe Gln Asp
 35 40 45
 Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
 50 55 60
 Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
 65 70 75 80
 Ile Lys His Thr Arg Thr Gln Glu Val His His Pro Ile Cys Ala Phe
 85 90 95
 Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly
 100 105 110

Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys	115	120	125
Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala	130	135	140
Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr	145	150	155
Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Thr	Leu	Leu	Thr	165	170	175
Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	180	185	190
Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	195	200	205
Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val	210	215	220
Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly	225	230	235
Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	245	250	255
Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu	260	265	270
Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu	275	280	285
Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys	290	295	300
Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe	305	310	315
Gly	Val	Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe	Ile	Val	Val	Met	Val	325	330	335
Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu	340	345	350
Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	355	360	365
Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile	370	375	380
Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Leu	Phe	385	390	395
Ile	Phe	Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp	405	410	415
Arg	Arg	His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Leu	Ala	Asp	Asn	Ser	Asp	420	425	430
Trp	Ser	Lys	Thr	Ala	Thr	Asn	Ile	Ile	Lys	Lys	Ser	Ser	Asp	Asn	Leu	435	440	445
Gly	Lys	Ser	Leu	Ser	Ser	Ser	Ser	Ile	Gly	Ser	Asn	Ser	Thr	Tyr	Leu	450	455	460
Thr	Ser	Lys	Ser	Lys	Ser	Ser	Ser	Thr	Thr	Tyr	Phe	Lys	Arg	Asn	Ser	465	470	475
His	Thr	Asp	Asn	Val	Ser	Tyr	Glu	His	Ser	Phe	Asn	Lys	Ser	Gly	Ser	485	490	495
Leu	Arg	Gln	Cys	Phe	His	Gly	Gln	Val	Leu	Val	Lys	Thr	Gly	Pro	Cys	500	505	510

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<211> 27

<212> DNA

<213> homo sapiens

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27

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<212> DNA
<213> homo sapiens

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atggcgtgca gtattggaaa cattactatc cagaatctga aggatcctgt tcaaataaaa 240
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gcaagtgaga cagtctgcct gtgtaaccac ttcacacact ttggagttct gatggacctt 420
ccaagaagtg cctcacagtt agatgcaaga aacactaaag tctcacttt catcagctat 480
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gagaaattgc gaagggatta tccctccaaa atcttgatga acctgagcac agcctgtctg 600
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<211> 403
<212> PRT
<213> homo sapiens

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35 40 45
Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
50 55 60
Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
65 70 75 80

Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His	Pro	Ile	Cys	Ala	Phe		
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Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly		
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Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys		
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Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala		
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Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr		
145					150					155					160		
Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala	Thr	Leu	Leu	Thr		
			165					170						175			
Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu		
		180						185					190				
Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu		
		195					200					205					
Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val		
	210					215					220						
Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly		
225				230					235					240			
Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr		
			245					250						255			
Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu		
		260						265					270				
Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu		
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Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys		
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Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe		
305					310					315					320		
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			325					330						335			
Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu		
			340					345					350				
Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu		
		355					360					365					
Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile		
	370					375					380						
Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Lys	Ile		
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<211> 3669

<212> DNA

<213> homo sapiens

<400> 33

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ataacattta	acgactttga	cattgaagaa	gctcccaatt	gcatttatga	ctcattatcc	300
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 <212> PRT
 <213> homo sapiens

<400> 34

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			20					25					30		
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65						70				75					80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
				35					90					95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
			100					105					110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
			115				120					125			
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135					140				
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
145					150					155					160
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
				165				170						175	
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
			180					185					190		
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
		195				200						205			
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
	210					215					220				
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
225					230					235					240
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
				245					250					255	
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
			260					265						270	
Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
		275					280					285			
Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
	290					295					300				
Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
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Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr
	370					375					380				
Arg	Ile	Ser	Val	Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys
385					390					395					400

Val	Gln	Ser	Lys	Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp
				405					410					415	
Asn	Tyr	Thr	Val	Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly
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Glu	Asp	Lys	Ile	Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu
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Val	Leu	Trp	Ala	Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu
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Asp	Glu	Gly	Leu	Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His
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Cys	Leu	Ala	Met	Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln
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Pro	Ser	Glu	Tyr	Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala
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Ser	Arg	Ile	Cys	Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp
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		660					665						670		
Pro	Ser	Asn	Asn	Glu	Ser	Tyr	Phe	Gln	Met	Asp	Phe	Glu	Ser	Gly	Gln
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Val	Asp	Pro	Leu	Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn
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Phe	Asn	Lys	Thr	Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr
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Leu	Val	Ser	Tyr	Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln
			740					745					750		
Asn	Leu	Lys	Asp	Pro	Val	Gln	Ile	Lys	Ile	Lys	His	Thr	Arg	Thr	Gln
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Glu	Val	His	His	Pro	Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys
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 Val Leu Ala Ser Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr
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<212> DNA

<213> homo sapiens

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 <213> homo sapiens

<400> 36

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			20					25					30		
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
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Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			85					90						95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
		100					105					110			
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
		115					120					125			
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135						140			
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
145				150					155						160
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
			165					170						175	
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
		180					185						190		
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
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Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys
225				230					235						240
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
			245					250						255	
Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
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Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
			325					330						335	
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
		340					345					350			
Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
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Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr
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Val	Gln	Ser	Lys	Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp
			405						410					415	
Asn	Tyr	Thr	Val	Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly
			420					425					430		
Glu	Asp	Lys	Ile	Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu
		435					440					445			
Val	Leu	Trp	Ala	Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu
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Glu	Gly	Lys	Ile	Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu
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Asp	Glu	Gly	Leu	Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His
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Thr	Ser	His	Val	Asn	Ile	Thr	Thr	Arg	Asn	Leu	Ala	Leu	Ser	Val	Ser
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Ser	Leu	Leu	Pro	Gly	Thr	Asn	Ala	Ile	Ser	Asn	Phe	Ser	Ile	Gly	Leu
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Pro	Ser	Asn	Glu	Ser	Tyr	Phe	Gln	Met	Asp	Phe	Glu	Ser	Gly	Gln	
		675					680				685				
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Phe	Asn	Lys	Thr	Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr
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785					790					795					800
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<211> 690

<212> PRT

<213> homo sapiens

<400> 38

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		20						25					30		
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
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Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			85					90					95		
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
		100					105					110			
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His

	565		570		575
Asn Ile Thr	Asn Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu				
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Glu Asn Ile Asp Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser					
	595		600		605
Asn Ile Leu Ser Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu					
	610		615		620
Ala Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser					
625		630		635	640
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			165				170						175		
Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly
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His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe
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Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	Ser
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225					230					235				240	
Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	Trp
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		260					265					270			
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Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys	Gly
	290					295					300				

Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys	Ile
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Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp	Gln
			325						330					335	
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		340					345						350		
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		355				360						365			
Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr	Arg
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Gln	Ser	Lys	Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn
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	435						440					445			
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Glu	Gly	Leu	Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys
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Gln	Ile	Leu	Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala	Asn
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	675						680					685			
Asp	Pro	Leu	Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn	Leu
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Val	Ser	Tyr	Val	Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn
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58

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 His Ser Thr Lys Phe
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<212> PRT

<213> homo sapiens

<400> 44

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			20					25					30		
Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro	Ser
			35				40						45		
Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	Gln
	50					55					60				
Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile
65					70					75				80	
Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp
				85					90					95	
Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	Ala
			100					105					110		
Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	Val
			115				120						125		
Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	Ser
	130					135					140				
Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	Pro
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Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile
				165					170					175	
Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly
			180					185					190		
His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe
		195				200						205			
Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	Ser
	210					215					220				
Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	Glu
225					230					235				240	
Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	Trp
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Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	Glu
			260					265						270	

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 740 745 750
 Leu Lys Asp Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu
 755 760 765
 Val His His Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser
 770 775 780
 Phe Gly Gly Trp Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser Asp
 785 790 795 800
 Ala Ser Glu Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val
 805 810 815
 Leu Met Asp Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr
 820 825 830
 Lys Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile
 835 840 845
 Phe Ser Ala Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu Arg
 850 855 860
 Arg Asp Tyr Pro Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu Leu
 865 870 875 880
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 885 890 895
 Val Asp Gly Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu
 900 905 910
 Leu Ala Thr Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile
 915 920 925
 Ala Leu Val Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys
 930 935 940
 Phe Cys Ile Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val
 945 950 955 960
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 965 970 975
 Lys Glu Lys Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe
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 Tyr Val Thr Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile
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 Ala Met Phe Ile Val Val Met Val Gln Ile Cys Gly Arg Asn Gly Lys
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 Arg Ser Asn Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser
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 Val Val Ser Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe
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 Lys Glu Asn Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg
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 Phe Arg Leu Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile
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 1125 1130 1135
 Ile Gly Ser Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser
 1140 1145 1150
 Thr Thr Tyr Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu
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 <212> PRT
 <213> homo sapiens

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Glu Gly Leu Arg	Leu His Thr Val	Asn Val Arg	Gln Leu Gly	His Cys		
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Leu Ala Met Glu	Pro Lys Gly Tyr	Trp Pro Ser	Ile Gln Pro			
	500		505		510	
Ser Glu Tyr Val	Leu Pro Cys Pro	Asp Lys Pro	Gly Phe Ser	Ala Ser		
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Arg Ile Cys Phe	Tyr Asn Ala Thr	Asn Pro Leu	Val Thr Tyr	Trp Gly		
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Pro Val Asp Ile	Ser Asn Cys Leu	Lys Glu Ala	Asn Glu Val	Ala Asn		
	545		550		555	
Gln Ile Leu Asn	Leu Thr Ala Asp	Gly Gln Asn	Leu Thr Ser	Ala Asn		
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Asn Ile Asp Ile	Thr Leu Gly Ser	Thr Leu Met	Asn Ile Phe	Ser Asn		
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	610		615		620	
Leu Lys Thr Ile	Asp Glu Leu Ala	Phe Lys Ile	Asp Leu Asn	Ser Thr		
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Ser His Val Asn	Ile Thr Thr Arg	Asn Leu Ala	Leu Ser Val	Ser Ser		
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<400> 47

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Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
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Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
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2040
2073

<210> 54
<211> 690
<212> PRT
<213> homo sapiens

<400> 54

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			20					25					30		
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
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Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			85					90						95	
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
		100					105					110			
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
	130					135						140			
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
				165				170						175	
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
		180					185						190		
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
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Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
			325						330					335	
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
	355						360					365			
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr

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385	390	395
Val Gln Ser Lys Val	Ala Glu Trp Leu Asn Ser	Thr Phe Gln Asn Trp
405	410	415
Asn Tyr Thr Val Tyr	Val Val Asn Ile Ser Phe	His Leu Ser Ala Gly
420	425	430
Glu Asp Lys Ile Lys	Val Lys Arg Ser Leu Glu	Asp Glu Pro Arg Leu
435	440	445
Val Leu Trp Ala Leu	Leu Val Tyr Asn Ala Thr	Asn Asn Thr Asn Leu
450	455	460
Glu Gly Lys Ile Ile	Gln Gln Lys Leu Leu Lys	Asn Asn Glu Ser Leu
465	470	475
Asp Glu Gly Leu Arg	Leu His Thr Val Asn Val	Arg Gln Leu Gly His
485	490	495
Cys Leu Ala Met Glu	Glu Pro Lys Gly Tyr Tyr	Trp Pro Ser Ile Gln
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Pro Ser Glu Tyr Val	Leu Pro Cys Pro Asp Lys	Pro Gly Phe Ser Ala
515	520	525
Ser Arg Ile Cys Phe	Tyr Asn Ala Thr Asn Pro	Leu Val Thr Tyr Trp
530	535	540
Gly Pro Val Asp Ile	Ser Asn Cys Leu Lys Glu	Ala Asn Glu Val Ala
545	550	555
Asn Gln Ile Leu Asn	Leu Thr Ala Asp Gly	Gln Asn Leu Thr Ser Ala
565	570	575
Asn Ile Thr Asn Ile	Val Glu Gln Val Lys Arg	Ile Val Asn Lys Glu
580	585	590
Glu Asn Ile Asp Ile	Thr Leu Gly Ser Thr Leu	Met Asn Ile Phe Ser
595	600	605
Asn Ile Leu Ser Ser	Ser Asp Ser Asp Leu Leu	Glu Ser Ser Ser Glu
610	615	620
Ala Leu Lys Thr Ile	Asp Glu Leu Ala Phe Lys	Ile Asp Leu Asn Ser
625	630	635
Thr Ser His Val Asn	Ile Thr Thr Arg Asn Leu	Ala Leu Ser Val Ser
645	650	655
Ser Leu Leu Pro Gly	Thr Asn Ala Ile Ser Asn	Phe Ser Ile Gly Leu
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690		

<210> 55

<211> 3255

<212> DNA

<213> homo sapiens

<400> 55

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<210> 56

<211> 1084

<212> PRT

<213> homo sapiens

<400> 56

Met Met Phe Arg Ser Asp Arg Met Trp Ser Cys His Trp Lys Trp Lys

1

5

10

15

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His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
		35					40					45			
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
	50					55					60				
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
65					70					75					80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			35					90					95		
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
		100						105					110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
		115					120					125			
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
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Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
		180						185					190		
Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
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225					230					235					240
Glu	Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val
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Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
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Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys
305				310					315						320
Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
			325					330					335		
Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
		355				360						365			
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Asp	Gly	Ile	Ile	Tyr
	370					375					380				
Arg	Ile	Ser	Val	Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys
385					390					395					400
Val	Gln	Ser	Lys	Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp
			405					410					415		
Asn	Tyr	Thr	Val	Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly
		420						425				430			
Glu	Asp	Lys	Ile	Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu
	435					440					445				
Val	Leu	Trp	Ala	Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu
	450					455					460				

Glu	Gly	Lys	Ile	Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu
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Asp	Glu	Gly	Leu	Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His
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Cys	Leu	Ala	Met	Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln
			500					505						510	
Pro	Ser	Glu	Tyr	Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala
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Ser	Arg	Ile	Cys	Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp
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Gly	Pro	Val	Asp	Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala
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Asn	Gln	Ile	Leu	Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala
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Asn	Ile	Thr	Asn	Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu
			580					585							590
Glu	Asn	Ile	Asp	Ile	Thr	Leu	Gly	Ser	Thr	Leu	Met	Asn	Ile	Phe	Ser
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Asn	Ile	Leu	Ser	Ser	Ser	Asp	Ser	Asp	Leu	Leu	Glu	Ser	Ser	Ser	Glu
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Ala	Leu	Lys	Thr	Ile	Asp	Glu	Leu	Ala	Phe	Lys	Ile	Asp	Leu	Asn	Ser
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Ser	Leu	Leu	Pro	Gly	Thr	Asn	Ala	Ile	Ser	Asn	Phe	Ser	Ile	Gly	Leu
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Pro	Ser	Asn	Asn	Glu	Ser	Tyr	Phe	Gln	Met	Asp	Phe	Glu	Ser	Gly	Gln
			675				680					685			
Val	Asp	Pro	Leu	Ala	Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn
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Asn	Leu	Lys	Asp	Pro	Val	Gln	Ile	Lys	Ile	Lys	His	Thr	Arg	Thr	Gln
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Glu	Val	His	His	Pro	Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys
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Ser	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly	Cys	Val	Ala	His	Arg	Asp	Ser
785					790					795					800
Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys	Asn	His	Phe	Thr	His	Phe	Gly
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Val	Leu	Met	Asp	Leu	Pro	Arg	Ser	Ala	Ser	Gln	Leu	Asp	Ala	Arg	Asn
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Thr	Lys	Val	Leu	Thr	Phe	Ile	Ser	Tyr	Ile	Gly	Cys	Gly	Ile	Ser	Ala
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Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	Asp	Gly	Trp	Ile	Thr	Ser	Phe
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Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile	165	170	175
Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly	180	185	190
His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe	195	200	205
Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	Ser	210	215	220
Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	Glu	225	230	235
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Pro	Val	Asp	Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	545	550	555
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Sequence Comparison A

RESULT 8
T71087
LOCUS T71087 520 bp mRNA linear EST 01-MAR-1995
DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:84101 5', mRNA sequence.
ACCESSION T71087
VERSION T71087.1 GI:685608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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clone is available royalty-free through LLNL ; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
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dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb, Uni-ZAP XR Vector; -5' adaptor sequence 5'
GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

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Best Local Similarity 99.6%; Pred. No. 2.8e-47;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 62 AAAACAATTGATGAATTGGCCTTCAAGATAGACCTAAATAGCACATCACATGTGAATATT 121

Qy 2023 acaactcggaacttggtctctcagcgtatcatccctgttaccagggacaaatgcaatttca 2082
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Db 122 ACAACTCGGAACCTGGCTCTCAGCGTATCATCCCTGTTACCAGGGACAAATGCAATTCA 181

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Db      252  CTGCCATTTTCTCAGCTGCAACTCTCCTGACATATGTTGCTTTTGAGAAGCTGCGCAGGG 311
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RESULT 8

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T71087
LOCUS      T71087          520 bp      mRNA      linear      EST 01-MAR-1995
DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
            IMAGE:84101 5', mRNA sequence.
ACCESSION  T71087
VERSION    T71087.1  GI:685608
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 520)
AUTHORS    Hillier,L , Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfsing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE      Generation and analysis of 280,000 human expressed sequence tags
JOURNAL    Genome Res. 6 (9), 807-828 (1996)
MEDLINE    97044478
COMMENT    Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estawatson.wustl.edu
            Insert Size: 592
            High quality sequence stops: 314 Source IMAGE Consortium, LLNL This
            clone is available royalty-free through LLNL ; contact the IMAGE
            Consortium (info@image.llnl.gov) for further information.
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            High quality sequence stop: 314.
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; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence 5'
GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

Query Match 6.0%; Score 225.4; DB 10; Length 520;
Best Local Similarity 99.6%; Pred. No. 2.8e-47;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   122 ACAACTCGGAACCTGGCTCTCAGCGTATCATCCCTGTTACCAGGGACAAATGCAATTTCA 181

Qy  2083 aattttagcattgggtcttccaagcaataatgaatcgattttccagat 2129
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Db   182 AATTTTAGCATTGGTCTTCCAAGCAATAATGAATCGTATTTCCAGGT 228

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